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Sequence Listing was accepted.

See attached Validation Report.

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217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=2; day=2; hr=15; min=29; sec=59; ms=922;]

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Application No: 10575374

Version No: 3.0

Input Set:

Output Set:

Started: 2010-01-20 15:19:46.905

Finished: 2010-01-20 15:19:49.644

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 739 ms

Total Warnings: 48

Total Errors: 1

No. of SeqIDs Defined: 68

Actual SeqID Count: 68

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)

Input Set:

Output Set:

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Total Warnings: 48
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Actual SeqID Count: 68

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (38) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Ecole Polytechnique Federale de Lausanne (EPFL)

<120> Method for identification of suitable fragmentation sites in a reporter protein

<130> PEPF001WO

<140> 10575374

<141> 2010-01-20

<150> US 34,404 JM-213

<151> 2003-10-09

<160> 68

<170> PatentIn version 3.1

<210> 1

<211> 672

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> modified_base

<222> (186)..(186)

<223> silent point mutation introduced to generate HindIII restriction site

<300>

<308> NCBI / NC_001136

<309> 2004-08-30

<400> 1

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aaagcatata aaaatagttc aggcactccg aaatacttgg ttggcgtggt tcgtaatcaa	240
cctaaggagg atgttttggc tctgggtcaat gattacggca ttgatatcgt ccaactgcac	300
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gtattttcaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt	420
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tctgactggg ttggaaggca agagagcccc gagagcttac attttatggt agctggtgga	540
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agcggaggtg tggagacaaa tgggtgtaaaa gactctaaca aaatagcaaa tttcgtcaaa 660

aatgctaaga aa 672

<210> 2

<211> 224

<212> PRT

<213> *Saccharomyces cerevisiae*

<300>

<308> NCBI / NC_001136

<309> 2004-08-30

<400> 2

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
50 55 60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met

165

170

175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu
 180 185 190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly
 195 200 205

Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
 210 215 220

<210> 3
 <211> 132
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> modified_base
 <222> (22)..(22)
 <223> point mutation

<400> 3
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 gtgcccaata ga 132

<210> 4
 <211> 44
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 4

Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val
 1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
 20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg
 35 40

<210> 5
 <211> 540
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 5
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aatagttcag gcaactccgaa atacttggtt ggcgtgtttc gtaatcaacc taaggaggat 120
gttttggtc tggatcaatga ttacggcatt gatatcgctc aactgcacgg agatgagtcg 180
tggcaagaat accaagagtt cctcggtttg ccagttatta aaagactcgt atttccaaaa 240
gactgcaaca tactactcag tgcagcttca cagaaacctc attcgtttat tcccttgttt 300
gattcagaag caggtgggac aggtgaactt ttggattgga actcgatttc tgactggggt 360
ggaaggcaag agagccccga gagcttacat tttatgttag ctggtggact gacgccagaa 420
aatgttggtg atgcgcttag attaaatggc gttattggtg ttgatgtaag cggaggtgtg 480
gagacaaatg gtgtaaaaga ctctaacaaa atagcaaatt tcgtcaaaaa tgctaagaaa 540

<210> 6
<211> 180
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 6

Lys Arg Thr Ile Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val
1 5 10 15

Lys Ala Tyr Lys Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val
20 25 30

Phe Arg Asn Gln Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr
35 40 45

Gly Ile Asp Ile Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr
50 55 60

Gln Glu Phe Leu Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys
65 70 75 80

Asp Cys Asn Ile Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe
85 90 95

Ile Pro Leu Phe Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp
100 105 110

Trp Asn Ser Ile Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser

115

120

125

Leu His Phe Met Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp
 130 135 140

Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val
 145 150 155 160

Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys
 165 170 175

Asn Ala Lys Lys
 180

<210> 7

<211> 159

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 7

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agcacagagg cgcagaaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120

gtgcccgaata gaaagagaac aattgacccg gttattgca 159

<210> 8

<211> 53

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 8

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
 1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
 20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
 35 40 45

Asp Pro Val Ile Ala
 50

<210> 9

<211> 516

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 9

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gcaaggaaaa tttcaagtct tgtaaaagct tataaaaata gttcaggcac tccgaaatac      60
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ggcattgata tcgtccaact gcacggagat gagtcgtggc aagaatacca agagttcctc      180
ggtttgccag ttattaaaag actcgtatct ccaaagact gcaacatact actcagtgca      240
gcttcacaga aacctcattc gtttattccc ttgtttgatt cagaagcagg tgggacaggt      300
gaacttttgg attggaactc gatttctgac tgggttgga ggcaagagag ccccgagagc      360
ttacatttta tgtagctgg tggactgacg ccagaaaatg ttggtgatgc gcttagatta      420
aatggcgtaa ttggtgttga tgtaagcgga ggtgtggaga caaatggtgt aaaagactct      480
aacaaaatag caaatctcgt caaaaatgct aagaaa                                516
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<210> 10

<211> 172

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 10

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Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys Asn Ser Ser Gly
1              5              10              15
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Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln Pro Lys Glu Asp
                20              25              30
```

```
Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile Val Gln Leu His
                35              40              45
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```
Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu Gly Leu Pro Val
                50              55              60
```

```
Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile Leu Leu Ser Ala
                65              70              75              80
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Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe Asp Ser Glu Ala
                85              90              95
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Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile Ser Asp Trp Val
                100             105             110
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Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met Leu Ala Gly Gly
115 120 125

Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu Asn Gly Val Ile
130 135 140

Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly Val Lys Asp Ser
145 150 155 160

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
165 170

<210> 11
<211> 561
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 11
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agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120
gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta 180
aaagcttata aaaatagttc aggcactccg aaatacttgg ttggcgtggt tcgtaatcaa 240
cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac 300
ggagatgagt cgtggcaaga ataccaagag ttcctcggtt tgccagttat taaaagactc 360
gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt 420
attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt 480
tctgactggg ttggaaggca agagagcccc gagagcttac attttatggt agctggtgga 540
ctgacgccag aaaatgttgg t 561

<210> 12
<211> 187
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 12

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
50 55 60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly
180 185

<210> 13
<211> 111
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 13
gatgcgctta gattaaatgg cgttattggt gttgatgtaa gcggaggtgt ggagacaaat 60
gggtgtaaaag actctaacaa aatagcaaat ttcgtcaaaa atgctaagaa a 111

<210> 14
<211> 37
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 14

Asp Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly
1 5 10 15

Val Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val
20 25 30

Lys Asn Ala Lys Lys
35

<210> 15

<211> 612

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> mutation

<222> (22)..(22)

<223> point mutation

<220>

<221> deletion

<222> (612)..(612)

<223> missing sequence after base 612 of wild-type: GAGACAAATGGTGTAAG
ACTCT

<400> 15

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agcacagagg cgcgagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120
gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta 180
aaagcttata aaaatagttc aggcactccg aaatacttgg ttggcgtggt tcgtaatcaa 240
cctaaggagg atgttttggc tctgggtcaat gattacggca ttgatatcgt ccaactgcac 300
ggagatgagt cgtggcaaga ataccaagag ttcctcgggt tgccagttat taaaagactc 360
gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt 420
attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttgattg gaactcgatt 480
tctgactggg ttggaaggca agagagcccc gagagcttac attttatggt agctggtgga 540
ctgacgccag aaaatgttgg tgatgcgctt agattaaatg gcgttattgg tgttgatgta 600
agcggaggtg tg 612

<210> 16
<211> 204
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 16

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1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
50 55 60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
130 135 140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145 150 155 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
165 170 175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu
180 185 190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val
195 200

<210> 17
 <211> 36
 <212> DNA
 <213> *Saccharomyces cerevisiae*

 <220>
 <221> mutation
 <222> (1)..(1)
 <223> missing sequence before base 1 of SEQ17, corresponding to base 63
 7 of wild-type: GAGACAAATGGTGTAAAAGACTCT

<400> 17
 aacaaaatag caaatctcgt caaaaatgct aagaaa 36

<210> 18
 <211> 12
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 18

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
 1 5 10

<210> 19
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> first of a pair of peptides (together with peptide C2), that asso-
 ciate into an anti-parallel coiled coil (Biochemistry 37 (1998),
 12603-12610)

<400> 19

Met Asp Tyr Lys Asp Glu Ser Gly Gln Ala Leu Glu Lys Glu Leu Ala
 1 5 10 15

Gln Asn Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Leu
 20 25 30

Glu Lys Glu Leu Gln Ala Gly Ser Gly Ser Gly
 35 40

<210> 20
 <211> 50
 <212> PRT
 <213> Artificial Sequence

<220>

<223> second of a pair of peptides (together with peptide C1), that associate into an anti-parallel coiled coil (Biochemistry 37 (1998), 12603-12610)

<400> 20

Gly Gly Ser Gly Ser Gly Gln Ala Leu Lys Lys Lys Leu Ala Gln Leu
1 5 10 15

Lys Trp Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Lys
20 25 30

Lys Leu Gln Ala Gly Ser Tyr Pro Tyr Asp